What Is Claimed Is:

1. A primer design system, comprising:

a receiver for obtaining data on a plurality of DNA nucleotide sequences from a first database having data on a plurality of different DNA nucleotide sequences; and

a control unit for controlling the system, said control unit controling:

extracting means for extracting partial sequences meeting certain base length extraction conditions from the plurality of DNA nucleotide sequences, the data for which were obtained by said receiver;

detecting means for detecting certain conditions related to the positions of said partial sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences;

first selecting means for selecting partial sequences meeting said conditions from said partial sequences based on the results of said detecting means; and

determining means for determining the nucleotide sequence of primers capable of specifically hybridizing to said plurality of DNA nucleotide sequences based on the results of said first selecting means.

2. A primer design system according to claim 1, said control unit further controls second selecting means for selecting DNA nucleotide sequences meeting certain selection conditions from the partial sequences extracted by said extracting means.

3. A primer design system according to claim 2, said selection conditions being related to GC content and/or Tm.

4. A primer design system according to claim 1, said control unit further controls limiting means for limiting the plurality of DNA nucleotide sequences, the data for which were obtained by said receiver, to a base length longer than said prescribed base length, to be output to said extracting means.

5. A primer design system according to claim 1, said control unit further controls of third selecting means for selecting DNA nucleotide sequences meeting selection conditions related to GC content and/or Tm based on the plurality of DNA nucleotide sequences, the data for which were obtained by said receiver.

6. A primer design system according to claim 1, further comprising a second database including data for a plurality of different DNA nucleotide sequences, said second database comprising at least one of either data on cDNA nucleotide sequences included in said first database,

or data on the exon nucleotide sequences predicted on the basis of genomic DNA nucleotide sequences included in said first database, wherein said extracting means targets nucleotide sequences included in said second database for extraction.

7. A storage medium having recorded thereon a program executable at a control unit in a computer having said control unit and memory with data on a plurality of different DNA nucleotide sequences, said program comprising instruction for reading data on a plurality of DNA nucleotide sequences in said memory, for extracting partial sequences having a prescribed base length from said nucleotide sequences based on data on said read plurality of DNA nucleotide sequences, for detecting certain conditions related to the positions of said partial sequences and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences, for selecting partial sequences meeting said conditions, and for determining the nucleotide sequences of primers capable of hybridizing specifically to said plurality of DNA nucleotide sequences based on said selected partial sequences.

8. A method for designing primers, comprising the steps of:

taking data on a plurality of DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences;

extracting partial sequences having a certain base length from said plurality of DNA nucleotide sequences based on said nucleotide sequence data obtained above;

detecting certain conditions related to the positions of said partial sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences;

selecting partial sequences meeting said conditions from said partial sequences based on said detecting results; and

determining the nucleotide sequences of primers capable of specifically hybridizing to said DNA nucleotide sequences based on said selected partial sequences.

9. A computer-readable storage medium used in bioinformatics, said storage medium comprising recorded data on a plurality of primers capable of specifically hybridizing to mutually different DNAs, and genetic data on DNA fragments amplified by PCR using said plurality of primers, which are correlated each other.

10. A computer-readable storage medium comprising data on a plurality of primers capable of specifically hybridizing to mutually different DNAs, and genetic data on DNA fragments amplified by PCR using said plurality of primers, which are collelated each other, as well as a recorded program for displaying on a display device genetic data on said DNA fragments corresponding to data on said plurality of primers input by means of input/output unit of a computer.

11. A method for analyzing DNA, comprising the analysis of sample DNA using as an indicator the type of primer affording PCR amplified fragments among said plurality of primers, using a DNA analysis kit comprising a storage medium according to claim 9 and a plurality of primers, the data for which have been recorded on said storage medium.

12. A DNA analysis kit, comprising a storage medium according to claim 9, and a plurality of primers for which said primer data are recorded.

13. Micro-well plates for PCR, comprising 75 or more types of solution comprising 1 or more primers.

14. Micro-well plates for PCR, comprising a plurality of solutions comprising 1 or more primers, the primer concentration in said solutions ranging between 10

and 100 pmol/μL, with no enzymes that degrade the primers in said solutions.

15. Micro-well plates for PCR, comprising a plurality of wells, 80% or more of the total of said plurality of wells containing mutually different solutions comprising 1 or more primers.

16. Micro-well plates for PCR according to claim 13, comprising the plurality of primers designed by means of a primer design method comprising the steps of: taking data on a plurality of DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences; limiting the base length of said plurality of DNA nucleotide sequences to a certain base length based on said nucleotide sequence data taken above; extracting first partial sequences having a certain base length from said limited nucleotide sequences; selecting second partial sequences meeting selection conditions related to GC content and/or Tm from said first partial sequences; detecting certain conditions related to the positions of said second partial sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences; selecting third partial sequences meeting said conditions from said second partial sequences based on said detectd results; and determining the nucleotide sequence of primers capable of specifically hybridizing

to said DNA nucleotide sequences based on said third partial sequences.

17. Micro-well plates for PCR according to claim 13, comprising a plurality of primers designed by means of a primer design method comprising the steps of: taking data on a plurality of DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences; selecting DNA nucleotide sequences meeting selection conditions related to GC content and/or Tm from a plurality of DNA nucleotide sequences, the data for which have been obtained above; extracting partial sequences having a certain base length from said selected nucleotide sequences; detecting certain conditions related to the positions of said partial sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences; selecting partial sequences meeting certain conditions from said partial sequences based on said detectd results; and determining the nucleotide sequence of primers capable of specifically hybridizing to said DNA nucleotide sequences based on said selected partial sequences.

18. A PCR amplifying kit comprising a plurality of primers and a computer-readable storage medium, said PCR amplifying kit comprising containers containing said plurality of primers, ID codes assigned to the primers contained in the containers being indicated on said

containers, and a table correllating said ID codes of said plurality of primers with either the name, molecular formula, or sequence data for said plurality of primers being recorded on said storage medium.

add B3

add C5

add E6

ADD F6